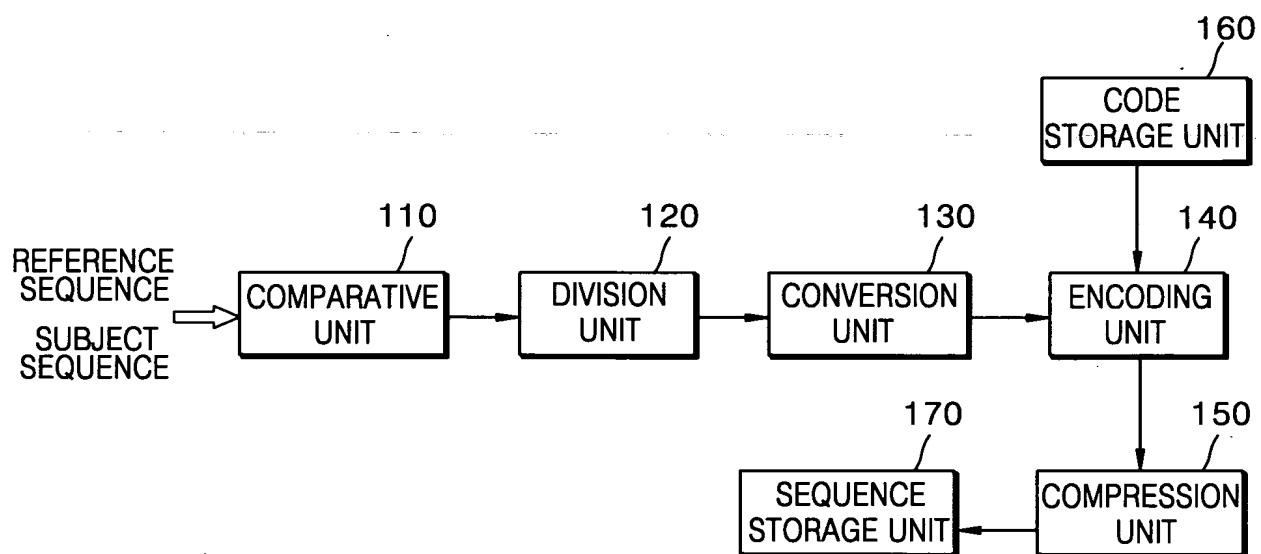


FIG. 1



7 -

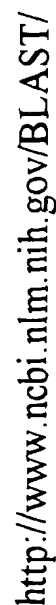
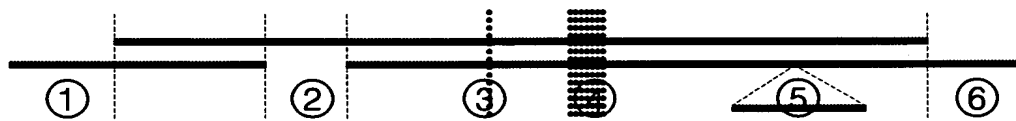
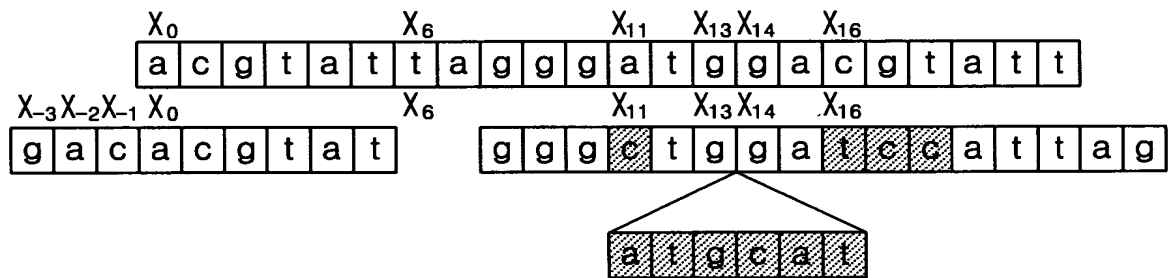


FIG. 3



- ① Start region mismatch
- ② Blank region
- ③ Single base pair mismatch
- ④ Multiple base pair mismatch
- ⑤ Inserted region
- ⑥ End region mismatch



$/-3 \sim 3gac/3/6/2/3 \sim 1c/1/1 \sim 6atgcat/1/2 \sim 3tcc/3/4 \sim 2ag/2$

FIG. 4

4BITS CODES FOR ENCODING INFORMATION ABOUT
THE DIFFERENCE BETWEEN DNA SEQUENCES

| | |
|----------|----------|
| 0 : 0000 | 8 : 1000 |
| 1 : 0001 | 9 : 1001 |
| 2 : 0010 | A : 1010 |
| 3 : 0011 | T : 1011 |
| 4 : 0100 | G : 1100 |
| 5 : 0101 | C : 1101 |
| 6 : 0110 | / : 1110 |
| 7 : 0111 | ~ : 1111 |

FIG. 5

MODY3 exons (5552 characters = 5552 byte)
ref|NT_028327.5|Hs12_28486 Homo sapiens chromosome 12 reference genomic contig
Length = 906100

| | | |
|----------------------|----------------------|----------------------|
| Exon2 /354759-1a/1 | Exon789 /363265-1V/1 | Exon789 /363384-1V/1 |
| Exon3 /359197-1V/1 | Exon789 /363261-1V/1 | Exon789 /363391-1V/1 |
| Exon456 /362119-1a/1 | Exon789 /363267-1V/1 | Exon789 /363394-1V/1 |
| Exon456 /362178-1a/1 | Exon789 /363273-1V/1 | Exon789 /363641-1a/1 |
| Exon789 /363208-1V/1 | Exon789 /363278-1V/1 | Exon789 /363689-1a/1 |

/354759-1a/1/4438-1a/1/2922-1a/1/59-1a/1/30-1a/53-1V/1/4-1V/1/2-1V/1/6-1V/1/5-1V/1/6
1V/1/7-1V/1/3-1V/1/247-1a/1/248-1a/1
122byte

111000110101010001110101100111100001101011100001111001000100001110001110000110101110000111100010100100100100010
11100001101011100001111001011001111000011010111000011110001100001110000110101110010100111110000110111100001
1110010011100001101111000011110001011100001111010111110000111100110111000011011110000111100101111000011011
1110000111100110111000011011110000111100111110000110111110000111100011110001111000011011111000011110001001000111
11100001101011100001111000100100100011100001101011100001

61byte

FIG. 6

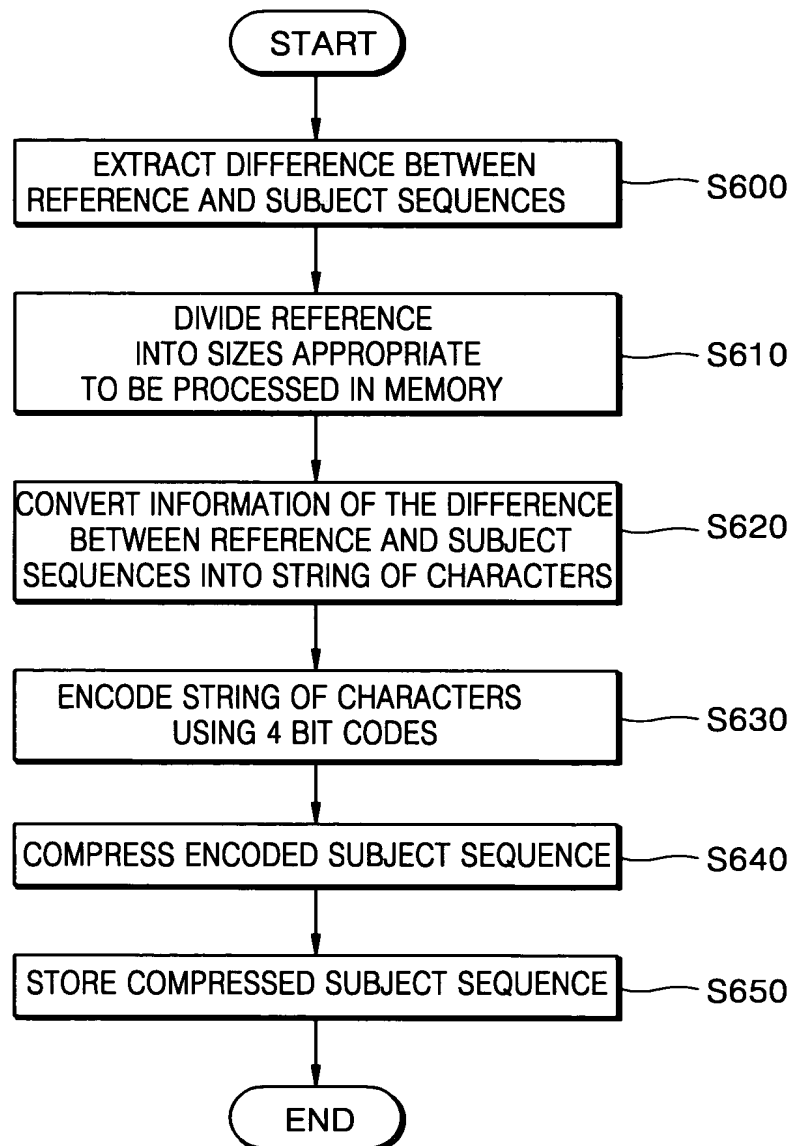


FIG. 7

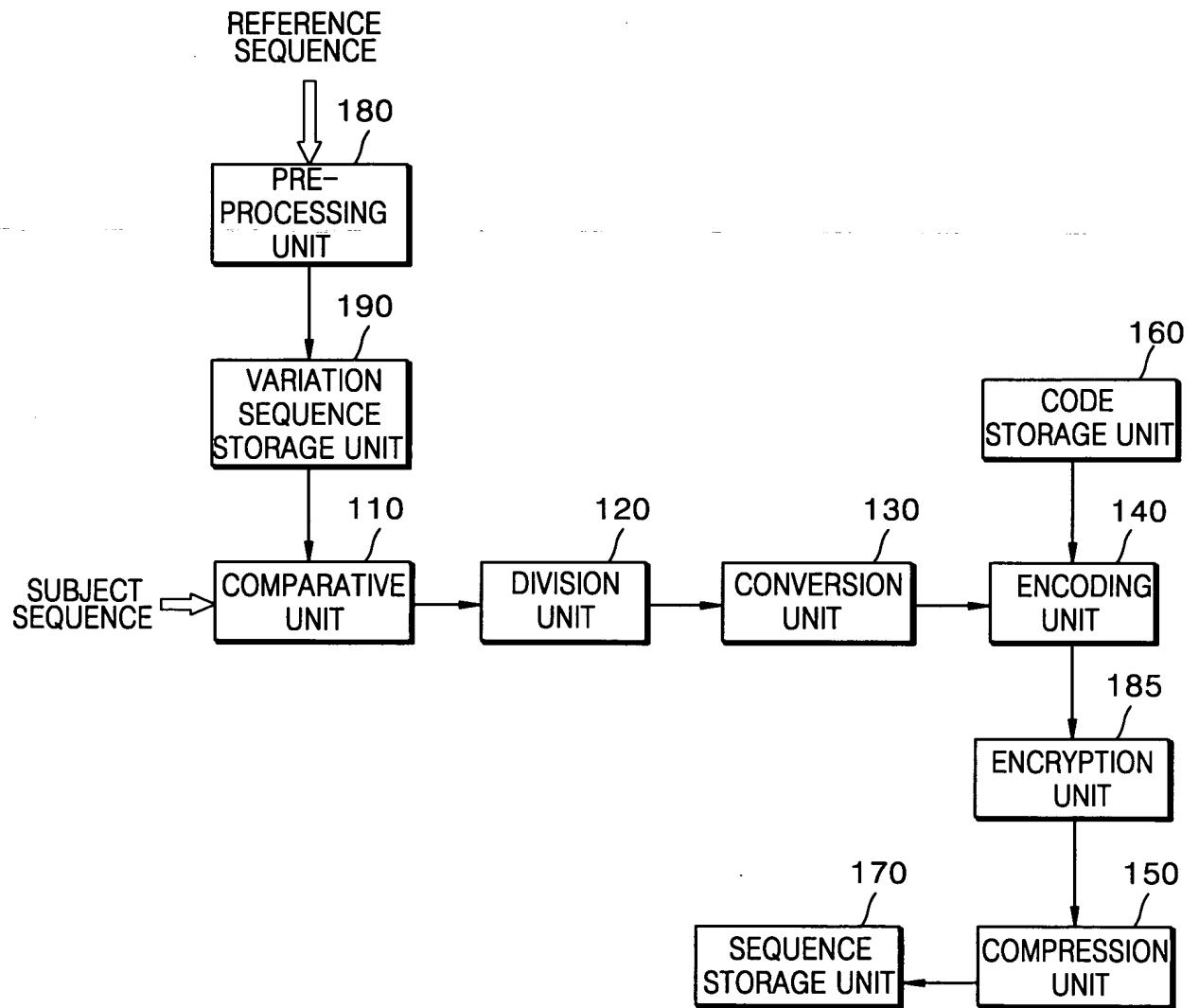


FIG. 8

TOTAL NUMBER OF VARIATION:4

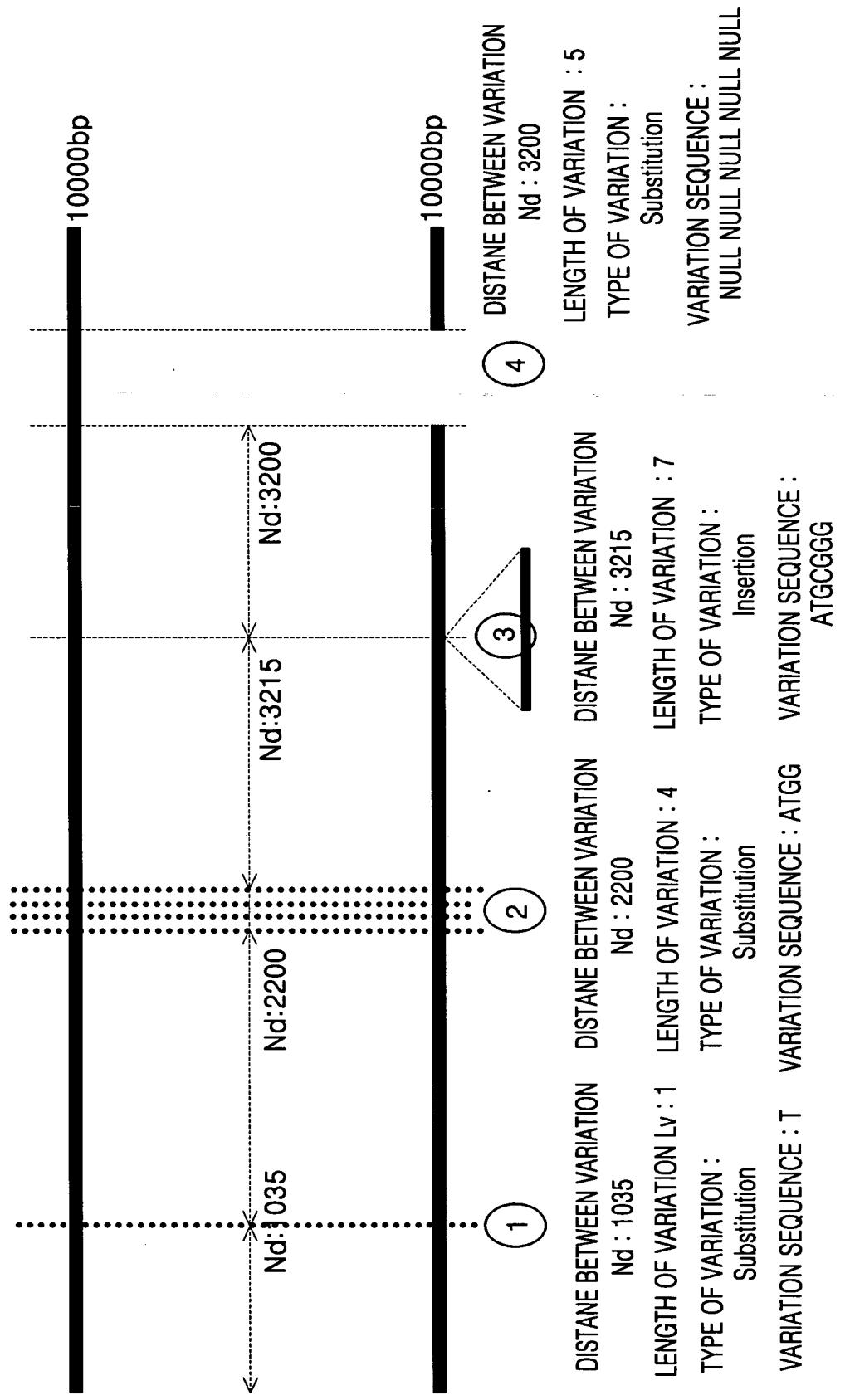


FIG. 9

